

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: LISA MCKERRACHER

(ii) TITLE OF INVENTION: Methods for making and delivering Rho-antagonist tissue adhesive formulations to the injured mammalian central and peripheral nervous systems and uses thereof

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BROULLETTE KOSIE
- (B) STREET: 1100 RENE-LESVEQUE BLVD WEST
- (C) PROV/STATE: QUEBEC
- (D) COUNTRY: CANADA
- (E) POSTAL/ZIP CODE: H3B 5C9

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE:ASCII (TEXT)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: BROULLETTE KOSIE
- (B) REGISTRATION NO.:
- (C) REFERENCE/DOCKET NO.: 06447-003-CA-2
- (D) TEL. NO.: (514) 397 8500
- (E) FAX NO.: (514) 397 8515

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(vii) IMMEDIATE SOURCE:

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

(A) AUTHORS:

(B) TITLE:

(C) JOURNAL:

(D) VOLUME:

(E) ISSUE:

(F) PAGES:

(G) DATE:

(H) DOCUMENT NO.:

(I) FILING DATE:

(J) PUBLICATION DATE:

(K) RELEVANT RESIDUES IN SEQ ID NO:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTG GCG ACC CTT CCC AAA TCG GAT CTG GTT CCG CGT GGA TCC TCT AGA  
1 5 10 15

GTC GAC CTG CAG GCA TGC AAT GCT TAT TCC ATT AAT CAA AAG GCT TAT TCA  
20 25 30

AAT ACT TAC CAG GAG TTT ACT AAT ATT GAT CAA GCA AAA GCT TGG GGT AAT  
35 40 45 50

GCT CAG TAT AAA AAG TAT GGA CTA AGC AAA TCA GAA AAA GAA GCT ATA  
55 60 65

GTA TCA TAT ACT AAA AGC GCT AGT GAA ATA AAT GGA AAG CTA AGA CAA  
 70 75 80

AAT AAG GGA GTT ATC AAT GGA TTT CCT TCA AAT TTA ATA AAA CAA GTT GAA  
 85 90 95

CTT TTA GAT AAA TCT TTT AAT AAA ATG AAG ACC CCT GAA AAT ATT ATG TTA  
 100 105 110 115

TTT AGA GGC GAC GAC CCT GCT TAT TTA GGA ACA GAA TTT CAA AAC ACT  
 120 125 130

CTT CTT AAT TCA AAT GGT ACA ATT AAT AAA ACG GCT TTT GAA AAG GCT AAA  
 135 140 145

GCT AAG TTT TTA AAT AAA GAT AGA CTT GAA TAT GGA TAT ATT AGT ACT TCA  
 150 155 160 165

TTA ATG AAT GTT TCT CAA TTT GCA GGA AGA CCA ATT ATT ACA AAA TTT AAA  
 170 175 180

GTA GCA AAA GGC TCA AAG GCA GGA TAT ATT GAC CCT ATT AGT GCT TTT CAG  
 185 190 195 200

GGA CAA CTT GAA ATG TTG CTT CCT AGA CAT AGT ACT TAT CAT ATA GAC GAT  
 205 210 215

ATG AGA TTG TCT TCT GAT GGT AAA CAA ATA ATA ATT ACA GCA ACA ATG  
 220 225 230

ATG GGC ACA GCT ATC AAT CCT AAA TAA  
 235 240

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGATCCTCTA GAGTCGACCT GCAGGCATGC AATGCTTATT CCATTAATCA 50  
AAAGGCTTAT TCAAATACCT ACCAGGAGTT TACTAATATT GATCAAGCAA 100  
AAGCTTGGGG TAATGCTCAG TATAAAAAGT ATGGACTAAG CAAATCAGAA 150  
AAAGAAGCTA TAGTATCATA TACTAAAAGC GCTAGTGAAA TAAATGGAAA 200  
GCTAAGACAA AATAAGGGAG TTATCAATGG ATTTCTTCA AATTAAATAA 250  
AACAAAGTTGA ACTTTAGAT AAATCTTTA ATAAAATGAA GACCCCTGAA 300  
AATATTATGT TATTTAGAGG CGACGACCCCT GCTTATTAG GAACAGAATT 350  
TCAAAACACT CTTCTTAATT CAAATGGTAC AATTAATAAA ACGGCTTTG 400  
AAAAGGCTAA AGCTAAGTTT TTAATAAAG ATAGACTTGA ATATGGATAT 450  
ATTAGTACTT CATTAATGAA TGTTTCTCAA TTTGCAGGAA GACCAATTAT 500  
TACAAAATTAAAGTAGCAA AAGGCTAAA GGCAGGATAT ATTGACCCCTA 550  
TTAGTGCTTT TCAGGGACAA CTTGAAATGT TGCTTCCTAG ACATAGTACT 600  
TATCATATAG ACGATATGAG ATTGTCTTCT GATGGTAAAC AAATAATAAT 650  
TACAGCAACAA ATGATGGGCA CAGCTATCAA TCCTAAATAA

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

(D) TOPOLOGY:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GSSRVDLQAC NAYSINQKAY SNTYQEFTNI DQAKAWGNAQ YKKYGLSKSE 50  
KEAIVSYTKS ASEINGKLRQ NKGVINGFPS NLIKQVELLD KSFNKMKTPE 100

NIMLFXGDDP AYLGTEFQNT LLNSNGTINK TAFEKAKAKF LNXDRLEYGY 150  
ISTSLMNVSQ FAGRPIITKF KVAKGSKAGY IDPISAFQGQ LEMLLPRHST 200  
YHIDDMRLSS DGKQIITAT MMGTAINPK